

SEQUENCE LISTING

(1) GENERAL INFORMATION

(i) APPLICANT: Hillman, Jennifer L.
Lal, Preeti
Corley, Neil C.
Shah, Purvi

(ii) TITLE OF THE INVENTION: NEW HUMAN PHOSPHATIDYLINOSITOL
(4,5) BISPHOSPHATE 5-PHOSPHATASE

(iii) NUMBER OF SEQUENCES: 5

(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: Incyte Genomics, Inc.
(B) STREET: 3160 Porter Drive
(C) CITY: Palo Alto
(D) STATE: CA
(E) COUNTRY: USA
(F) ZIP: 94304

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Diskette
(B) COMPUTER: IBM Compatible
(C) OPERATING SYSTEM: DOS
(D) SOFTWARE: FastSEQ for Windows Version 2.0

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER: To Be Assigned
(B) FILING DATE: Filed Herewith

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: 09/258,643; 08/884,681
(B) FILING DATE: February 26, 1999; June 27, 1997

(viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: Eckstrom, Richard A.
(B) REGISTRATION NUMBER: 37,027
(C) REFERENCE/DOCKET NUMBER: PF-0334-2 DIV

(ix) TELECOMMUNICATION INFORMATION:

(A) TELEPHONE: 650-855-0555
(B) TELEFAX: 650-845-4166

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 372 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

(A) LIBRARY: BRSTNOT03
(B) CLONE: 638789

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

Met Asp Val Leu Ser Pro Leu Ser Phe Ile Lys Val Ser His Val Arg
1 5 10 15
Met Gln Gly Ile Leu Leu Val Phe Ala Lys Tyr Gln His Leu Pro
20 25 30
Tyr Ile Gln Ile Leu Ser Thr Lys Ser Thr Pro Thr Gly Leu Phe Gly
35 40 45
Tyr Trp Gly Asn Lys Gly Gly Val Asn Ile Cys Leu Lys Leu Tyr Gly

50 55 60
Tyr Tyr Val Ser Ile Ile Asn Cys His Leu Pro Pro His Ile Ser Asn
65 70 75 80
Asn Tyr Gln Arg Leu Glu His Phe Asp Arg Ile Leu Glu Met Gln Asn
85 90 95
Cys Glu Gly Arg Asp Ile Pro Asn Ile Leu Asp His Asp Leu Ile Ile
100 105 110
Trp Phe Gly Asp Met Asn Phe Arg Ile Glu Asp Phe Gly Leu His Phe
115 120 125
Val Arg Glu Ser Ile Lys Asn Arg Cys Tyr Gly Gly Leu Trp Glu Lys
130 135 140
Asp Gln Leu Ser Ile Ala Lys Lys His Asp Pro Leu Leu Arg Glu Phe
145 150 155 160
Gln Glu Gly Arg Leu Leu Phe Pro Pro Thr Tyr Lys Phe Asp Arg Asn
165 170 175
Ser Asn Asp Tyr Asp Thr Ser Glu Lys Lys Arg Lys Pro Ala Trp Thr
180 185 190
Asp Arg Ile Leu Trp Arg Leu Lys Arg Gln Pro Cys Ala Gly Pro Asp
195 200 205
Thr Pro Ile Pro Pro Ala Ser His Phe Ser Leu Ser Leu Arg Gly Tyr
210 215 220
Ser Ser His Met Thr Tyr Gly Ile Ser Asp His Lys Pro Val Ser Gly
225 230 235 240
Thr Phe Asp Leu Glu Leu Lys Pro Leu Val Ser Ala Pro Leu Ile Val
245 250 255
Leu Met Pro Glu Asp Leu Trp Thr Val Glu Asn Asp Met Met Val Ser
260 265 270
Tyr Ser Ser Thr Ser Asp Phe Pro Ser Ser Pro Trp Asp Trp Ile Gly
275 280 285
Leu Tyr Lys Val Gly Leu Arg Asp Val Asn Asp Tyr Val Ser Tyr Ala
290 295 300
Trp Val Gly Asp Ser Lys Val Ser Cys Ser Asp Asn Leu Asn Gln Val
305 310 315 320
Tyr Ile Asp Ile Ser Asn Ile Pro Thr Thr Glu Asp Glu Phe Leu Leu
325 330 335
Cys Tyr Tyr Ser Asn Ser Leu Arg Ser Val Val Gly Ile Ser Arg Pro
340 345 350
Phe Gln Ile Pro Pro Gly Ser Leu Arg Glu Asp Pro Leu Gly Glu Ala
355 360 365
Gln Pro Gln Ile
370

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2573 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: BRSTNOT03
(B) CLONE: 638789

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

GAAGGCTCAG	CATACACGTC	GTGACTTGGA	ACGTGGCTTC	GGCAGCGCCC	CTCGAGCTCT	60
CAGTGACCTG	CTTCAGCTGA	ACAACCGGAA	CCTCAATCTT	GACATATATG	TTATTGGTTT	120
GCAGGAATTG	AACTCTGGGA	TCATAAGCCT	CCTTTCCGAT	GCTGCCTTTA	ATGACTCGTG	180
GAGCAGTTTC	CTCATGGATG	TGCTTTCCCC	TCTGAGCTTC	ATCAAGGTCT	CCCATGTCCG	240
TATGCAGGGG	ATCCTCTTAC	TGGTCTTTGC	CAAGTATCAG	CATTTGCCCT	ATATCCAGAT	300
TCTGTCTACT	AAATCCACCC	CCACTGGCCT	GTTTGGGTAC	TGGGGGAACA	AAGGTGGAGT	360
CAACATCTGC	CTGAAGCTTT	ATGGCTACTA	TGTCAGCATC	ATCAACTGCC	ACCTGCCCTC	420
CCACATTTCC	AACAATTACC	AGCGGCTGGA	GCACTTTGAC	CGGATCCTGG	AGATGCAGAA	480
TTGTGAGGGG	CGAGACATCC	CAAACATCCT	GGACCACGAC	CTCATTATCT	GGTTTGGAGA	540
CATGAACCTT	CGGATCGAGG	ACTTTGGGTT	GCACTTTGTT	CGGGAATCCA	TTAAAAATCG	600

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GTGCTACGGT GGCCTGTGGG AGAAGGACCA GCTCAGCATT GCCAAGAAAC ATGACCCGCT 660
GCTCCGGGAG TTCCAGGAGG GCCGCCTACT CTTCCCGCCC ACCTACAAGT TTGATAGGAA 720
CTCCAACGAC TATGACACCA GTGAGAAAAA ACGCAAGCCT GCATGGACCG ATCGCATCCT 780
GTGGAGGCTG AAGCGGCAGC CCTGTGCTGG CCCCACACT CCCATACCGC CGGCGTCACA 840
CTTCTCCTTG TCTCTGAGGG GCTACAGCAG CCACATGACG TACGGCATCA GCGACCACAA 900
GCCTGTCTCC GGCACGTTCG ACTTGGAGCT GAAGCCATTG GTGTCTGCTC CGCTGATCGT 960
CCTGATGCCC GAGGACCTGT GGACCGTGGA AAATGACATG ATGGTCAGCT ACTCTTCAAC 1020
CTCGGACTTC CCCAGCAGCC CGTGGGACTG GATTGGACTG TACAAGGTGG GGCTGCGGGA 1080
CGTTAATGAC TACGTGTCTT ATGCCCTGGGT CGGGGACAGC AAGGTCTCCT GCAGCGACAA 1140
CCTGAACCAG GTTTACATCG ACATCAGCAA TATCCCTACC ACTGAAGATG AGTTTCTCCT 1200
CTGTTACTAC AGCAACAGTC TGCCTTCTGT GGTGGGGATA AGCAGACCCT TCCAGATCCC 1260
GCCTGGCTCC TTGAGGGAGG ACCCACTGGG TGAAGCACAG CCACAGATCT GAGCCAGGAT 1320
GGGAGTGAAT CCCAGGCGGA GGCCAGAGCT GGCAGCCAGC TCTGCCTTTC CACTGCCGGG 1380
AGTGCTGGGG GCCCAGCCTG GCCCCCTGAA GAGACAGCCA AGTGTCGTCC ACATACTCCT 1440
CCCAGAGTGA GCTCTAACCA GGCTCATTTG CTCTCTCCAC TACTCATCTC TGGAAATTAGC 1500
CGCTTAAATA CAGGTTTTTTG TTGCTGAGAT GTGAGTGAAA CCAGCTAGTG TGTCAACAGT 1560
GAAGACCTGG GGACAGTTCT GCGTCTCATT TCTGGATTCC TACCCCTCTT TCTAGTCTTG 1620
CCCAAGTAGT CCTGCCAGGC ACATGCCCCA TTTGGCACAG GCCTGCATTC TTGTCGTGCC 1680
GTCCTGGGCC TCAGGCTGTC TGGGAGGGGA GATGCTCACA TTTGTACAGG CTACATAGAC 1740
TGGTGCAAGC AGTGCTGGAT TCCAGGAGTC TTGGCATCTC ATAGCTTGTC CCCGTGAGGA 1800
GTGAGCAGAG GGTCTGGGAT TTCTGCTTTC AGCAAAAGCA GTCTGACTCA GTGGGCAGAA 1860
TGGAGGGGCC CCTCTAGCCA GGCTCTTACG CCATGGTTAT GAGCAGGTTG ATGAGGGTCC 1920
TTCGGCCAGC ACAACCTTCC TCCCTACTCA CGGCATGGAG TCTGACTGCA TGGAAGTTCC 1980
AGATCCTGAC AGAGAGAACT GGGAAGGATC CAGGTTGCTT TCCGTTGGTA GCTTGAGTCC 2040
CATGCCTCCA CCCTGCCATC TGAGGAAGGG GTGACAAGTG GTCAAGGAGC TGTGGCCACA 2100
GACTTTTCCA GGGTGGTCTT TGGCAGGTGA GGTGCGTCTG TGCCACCCTT GTCAGGAGTC 2160
ATTGACGACG GGCCCCCCTT GGACCCCTCG GACCTCAGA GTGGGGGCAG GCAGAAGGGA 2220
GAACCAGCTC AAGACATTTT GGAGGATCTG GCCCTGGGGT TCTTCAGAGA ACACCCTCTA 2280
GGGGCTTTGG GGACATGGCC TGTCCCCACA TCCAGCACTT GCCTCCGCCA TGGTCACTCG 2340
GCAGCCCTTT TCCCAGGAGA AGACACCTCT GGGAGCCTGC TCAGTGCTTG TCCTGCCATC 2400
CTGTGTCTCT GGACTGAGGG TTACTCCAGT TGCTCTGTGT TGCATACTCT CCCCCGCAAG 2460
CCTGTGTATG AAGAATTGTC CCCTGGCTTC CAGCAGGCCA TGGCTGGCTG TTTTGTGACT 2520
GTTACATTGT GCAGGGGTAA TTATTAGCGT GGCTTTTACA CTTAAAAAAA AAA 2573

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(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 329 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: GenBank
- (B) CLONE: 1399101

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

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Ala Gly Leu Phe Gly Tyr Trp Gly Asn Lys Gly Gly Val Asn Ile Cys
 1           5           10           15

Leu Lys Leu Tyr Gly Tyr Tyr Val Ser Ile Ile Asn Cys His Leu Pro
          20           25           30

Pro His Ile Ser Asn Asn Tyr Gln Arg Leu Glu His Phe Asp Arg Ile
          35           40           45

Leu Glu Met Gln Asn Cys Glu Gly Arg Asp Ile Pro Asn Ile Leu Asp
          50           55           60

His Asp Leu Ile Ile Trp Phe Gly Asp Met Asn Phe Arg Ile Glu Asp
          65           70           75           80

Phe Gly Leu His Phe Val Arg Glu Ser Ile Lys Asn Arg Cys Tyr Gly
          85           90           95

Gly Leu Trp Glu Lys Asp Gln Leu Ser Ile Ala Lys Lys His Asp Pro
          100          105          110

Leu Leu Arg Glu Phe Gln Glu Gly Arg Leu Leu Phe Pro Pro Thr Tyr
          115          120          125

Lys Phe Asp Arg Asn Ser Asn Asp Tyr Asp Thr Ser Glu Lys Lys Arg

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130	135	140
Lys Pro Ala Trp Thr Asp Arg Ile Leu Trp Arg Leu Lys Arg Gln Pro		
145	150	155
Cys Ala Gly Pro Asp Thr Pro Ile Pro Pro Ala Ser His Phe Ser Leu		
	165	170
Ser Leu Arg Gly Tyr Ser Ser His Met Thr Tyr Gly Ile Ser Asp His		
	180	185
Lys Pro Val Ser Gly Thr Phe Asp Leu Glu Leu Lys Pro Leu Val Ser		
	195	200
Ala Pro Leu Ile Val Leu Met Pro Glu Asp Leu Trp Thr Val Glu Asn		
	210	215
Asp Met Met Val Ser Tyr Ser Ser Thr Ser Asp Phe Pro Ser Ser Pro		
225	230	235
Trp Asp Trp Ile Gly Leu Tyr Lys Val Gly Leu Arg Asp Val Asn Asp		
	245	250
Tyr Val Ser Tyr Ala Trp Val Gly Asp Ser Lys Val Ser Cys Ser Asp		
	260	265
Asn Leu Asn Gln Val Tyr Ile Asp Ile Ser Asn Ile Pro Thr Thr Glu		
	275	280
Asp Glu Phe Leu Leu Cys Tyr Tyr Arg Asn Ser Leu Arg Ser Val Val		
290	295	300
Gly Ile Arg Arg Pro Phe Gln Ile Pro Pro Gly Ser Leu Arg Glu Asp		
305	310	315
Pro Leu Gly Glu Ala Gln Pro Gln Ile		
	325	

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 942 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: GenBank
- (B) CLONE: 1019103

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Val Thr Val Pro Glu Pro Gly Ala Ala Glu Ser Arg Ala Pro Cys Gly	
1	5
Asp Ser Ser Gly Gly Cys Val Arg Ser Ala Gly Ala Ser Met Asp Gln	
	20
Ser Val Ala Ile Gln Glu Thr Leu Ala Glu Gly Glu Tyr Cys Val Ile	
	35
Ala Val Gln Gly Val Leu Cys Glu Gly Asp Ser Arg Gln Ser Arg Leu	
	50
Leu Gly Leu Val Arg Tyr Arg Leu Glu His Gly Gly Gln Glu His Ala	
65	70
Leu Phe Leu Tyr Thr His Arg Arg Met Ala Ile Thr Gly Asp Asp Val	
	85
Ser Leu Asp Gln Ile Val Pro Val Ser Arg Asp Phe Thr Leu Glu Glu	
	100
Val Ser Pro Asp Gly Glu Leu Tyr Ile Leu Gly Ser Asp Val Thr Val	
	115
Gln Leu Asp Thr Ala Glu Leu Ser Leu Val Phe Gln Leu Pro Phe Gly	
	130
Ser Gln Thr Arg Met Phe Leu His Glu Val Ala Arg Ala Cys Pro Gly	
145	150
Phe Asp Ser Ala Thr Arg Asp Pro Glu Phe Leu Trp Leu Ser Arg Tyr	
	165
Arg Cys Ala Glu Leu Glu Leu Glu Met Pro Thr Pro Arg Gly Cys Asn	
	180
Ser Ala Leu Val Thr Trp Pro Gly Tyr Ala Thr Ile Gly Gly Gly Gly	
	195
	200
	205

Ser	Asn	Phe	Asp	Gly	Leu	Arg	Pro	Asn	Gly	Lys	Gly	Val	Pro	Met	Asp
210						215					220				
Gln	Ser	Ser	Arg	Gly	Gln	Asp	Lys	Pro	Glu	Ser	Leu	Gln	Pro	Arg	Gln
225					230					235					240
Asn	Lys	Ser	Lys	Ser	Glu	Ile	Thr	Asp	Met	Val	Arg	Ser	Ser	Thr	Ile
				245					250					255	
Thr	Val	Ser	Asp	Lys	Ala	His	Ile	Leu	Ser	Met	Gln	Lys	Phe	Gly	Leu
			260					265					270		
Arg	Asp	Thr	Ile	Val	Lys	Ser	His	Leu	Leu	Gln	Lys	Glu	Glu	Asp	Tyr
		275					280					285			
Thr	Tyr	Ile	Gln	Asn	Phe	Arg	Phe	Phe	Ala	Gly	Thr	Tyr	Asn	Val	Asn
	290					295					300				
Gly	Gln	Ser	Pro	Lys	Glu	Cys	Leu	Arg	Leu	Trp	Leu	Ser	Asn	Gly	Ile
305					310					315					320
Gln	Ala	Pro	Asp	Val	Tyr	Cys	Val	Gly	Phe	Gln	Glu	Leu	Asp	Leu	Ser
				325					330					335	
Lys	Glu	Ala	Phe	Phe	Phe	His	Asp	Thr	Pro	Lys	Glu	Glu	Glu	Trp	Phe
			340					345					350		
Lys	Ala	Val	Ser	Glu	Gly	Leu	His	Pro	Asp	Ala	Lys	Tyr	Ala	Lys	Val
		355					360					365			
Lys	Leu	Ile	Arg	Leu	Val	Gly	Ile	Met	Leu	Leu	Leu	Tyr	Val	Lys	Gln
	370					375					380				
Glu	His	Ala	Ala	Tyr	Ile	Ser	Glu	Val	Glu	Ala	Glu	Thr	Val	Gly	Thr
385					390					395					400
Gly	Ile	Met	Gly	Arg	Met	Gly	Asn	Lys	Gly	Gly	Val	Ala	Ile	Arg	Phe
				405					410					415	
Gln	Phe	His	Asn	Thr	Ser	Ile	Cys	Val	Val	Asn	Ser	His	Leu	Ala	Ala
			420					425					430		
His	Ile	Glu	Glu	Tyr	Glu	Arg	Arg	Asn	Gln	Asp	Tyr	Lys	Asp	Ile	Cys
			435					440				445			
Ser	Arg	Met	Gln	Phe	Cys	Gln	Pro	Asp	Pro	Ser	Leu	Pro	Pro	Leu	Thr
	450					455					460				
Ile	Ser	Asn	His	Asp	Val	Ile	Leu	Trp	Leu	Gly	Asp	Leu	Asn	Tyr	Arg
465					470					475					480
Ile	Glu	Glu	Leu	Asp	Val	Glu	Lys	Val	Lys	Lys	Leu	Ile	Glu	Glu	Lys
				485					490					495	
Asp	Phe	Gln	Met	Leu	Tyr	Ala	Tyr	Asp	Gln	Leu	Lys	Ile	Gln	Val	Ala
			500					505					510		
Ala	Lys	Thr	Val	Phe	Glu	Gly	Phe	Thr	Glu	Gly	Glu	Leu	Thr	Phe	Gln
		515					520					525			
Pro	Thr	Tyr	Lys	Tyr	Asp	Thr	Gly	Ser	Asp	Asp	Trp	Asp	Thr	Ser	Glu
		530				535					540				
Lys	Cys	Arg	Ala	Pro	Ala	Trp	Cys	Asp	Arg	Ile	Leu	Trp	Lys	Gly	Lys
545					550					555					560
Asn	Ile	Thr	Gln	Leu	Ser	Tyr	Gln	Ser	His	Met	Ala	Leu	Lys	Thr	Ser
				565					570					575	
Asp	His	Lys	Pro	Val	Ser	Ser	Val	Phe	Asp	Ile	Gly	Val	Arg	Val	Val
			580					585				590			
Asn	Asp	Glu	Leu	Tyr	Arg	Lys	Thr	Leu	Glu	Glu	Ile	Val	Arg	Ser	Leu
		595					600					605			
Asp	Lys	Met	Glu	Asn	Ala	Asn	Ile	Pro	Ser	Val	Ser	Leu	Ser	Lys	Arg
	610					615					620				
Glu	Phe	Cys	Phe	Gln	Asn	Val	Lys	Tyr	Met	Gln	Leu	Lys	Val	Glu	Ser
625					630					635					640
Phe	Thr	Ile	His	Asn	Gly	Gln	Val	Pro	Cys	His	Phe	Glu	Phe	Ile	Asn
				645					650					655	
Lys	Pro	Asp	Glu	Ser	Tyr	Cys	Lys	Gln	Trp	Leu	Asn	Ala	Asn	Pro	
			660				665					670			
Ser	Arg	Gly	Phe	Leu	Leu	Pro	Asp	Ser	Asp	Val	Glu	Ile	Asp	Leu	Glu
		675					680					685			
Leu	Phe	Val	Asn	Lys	Thr	Thr	Ala	Thr	Lys	Leu	Asn	Ser	Gly	Glu	Asp
		690				695					700				
Lys	Ile	Glu	Asp	Ile	Leu	Val	Leu	His	Leu	Asp	Arg	Gly	Lys	Asp	Tyr
705					710					715					720
Phe	Leu	Ser	Val	Ser	Gly	Asn	Tyr	Leu	Pro	Ser	Cys	Phe	Gly	Ser	Pro
				725					730					735	

09092287 062601

Ile His Thr Leu Cys Tyr Met Arg Glu Pro Ile Leu Asp Leu Pro Leu
 740 745 750
 Glu Thr Ile Ser Glu Leu Thr Leu Met Pro Val Trp Thr Gly Asp Asp
 755 760 765
 Gly Ser Gln Leu Asp Ser Pro Met Glu Ile Pro Lys Glu Leu Trp Met
 770 775 780
 Met Val Asp Tyr Leu Tyr Arg Asn Ala Val Gln Glu Asp Leu Phe
 785 790 795 800
 Gln Gln Pro Gly Leu Arg Ser Glu Phe Glu His Ile Arg Asp Cys Leu
 805 810 815
 Asp Thr Gly Met Ile Asp Asn Leu Ser Ala Ser Asn His Ser Val Ala
 820 825 830
 Glu Ala Leu Leu Phe Leu Glu Ser Leu Pro Glu Pro Val Ile Cys
 835 840 845
 Tyr Ser Thr Tyr His Asn Cys Leu Glu Cys Ser Gly Asn Tyr Thr Ala
 850 855 860
 Ser Lys Gln Val Ile Ser Thr Leu Pro Ile Phe His Lys Asn Val Phe
 865 870 875 880
 His Tyr Leu Met Ala Phe Leu Arg Glu Leu Lys Asn Ser Ala Lys
 885 890 895
 Asn His Leu Asp Glu Asn Ile Leu Ala Ser Ile Phe Gly Ser Leu Leu
 900 905 910
 Leu Arg Asn Pro Ala Gly His Gln Lys Leu Asp Met Thr Glu Lys Lys
 915 920 925
 Lys Ala Gln Glu Phe Ile His Gln Phe Leu Cys Asn Pro Leu
 930 935 940

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 901 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: GenBank
- (B) CLONE: 1420920

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

Met Glu Pro Pro Leu Pro Val Gly Ala Gln Pro Leu Ala Thr Val Glu
 1 5 10 15
 Gly Met Glu Met Lys Gly Pro Leu Arg Glu Pro Cys Ala Leu Thr Leu
 20 25 30
 Ala Gln Arg Asn Gly Gln Tyr Glu Leu Ile Ile Gln Leu His Glu Lys
 35 40 45
 Glu Gln His Val Gln Asp Ile Ile Pro Ile Asn Ser His Phe Arg Cys
 50 55 60
 Val Gln Glu Ala Glu Glu Thr Leu Leu Ile Asp Ile Ala Ser Asn Ser
 65 70 75 80
 Gly Cys Lys Ile Arg Val Gln Gly Asp Trp Ile Arg Glu Arg Arg Phe
 85 90 95
 Glu Ile Pro Asp Glu Glu His Cys Leu Lys Phe Leu Ser Ala Val Leu
 100 105 110
 Ala Ala Gln Lys Ala Gln Ser Gln Leu Leu Val Pro Glu Gln Lys Asp
 115 120 125
 Ser Ser Ser Trp Tyr Gln Lys Leu Asp Thr Lys Asp Lys Pro Ser Val
 130 135 140
 Phe Ser Gly Leu Leu Gly Phe Glu Asp Asn Phe Ser Ser Met Asn Leu
 145 150 155 160
 Asp Lys Lys Ile Asn Ser Gln Asn Gln Pro Thr Gly Ile His Arg Glu
 165 170 175
 Pro Pro Pro Pro Pro Phe Ser Val Asn Lys Met Leu Pro Arg Glu Lys
 180 185 190
 Glu Ala Ser Asn Lys Glu Gln Pro Lys Val Thr Asn Thr Met Arg Lys

58

Val	Pro	Leu	Asp	Glu	Gly	Ala	Ser	Glu	Arg	Pro	Leu	Gln	Val	Pro	Lys
				725					730						735
Glu	Ile	Trp	Leu	Leu	Val	Asp	His	Leu	Phe	Lys	Tyr	Ala	Cys	His	Gln
			740					745					750		
Glu	Asp	Leu	Phe	Gln	Thr	Pro	Gly	Met	Gln	Glu	Glu	Leu	Gln	Gln	Ile
		755					760					765			
Ile	Asp	Cys	Leu	Asp	Thr	Ser	Ile	Pro	Glu	Thr	Ile	Pro	Gly	Ser	Asn
	770					775					780				
His	Ser	Val	Ala	Glu	Ala	Leu	Leu	Ile	Phe	Leu	Glu	Ala	Leu	Pro	Glu
785					790					795					800
Pro	Val	Ile	Cys	Tyr	Glu	Leu	Tyr	Gln	Arg	Cys	Leu	Asp	Ser	Ala	Tyr
			805						810					815	
Asp	Pro	Arg	Ile	Cys	Arg	Gln	Val	Ile	Ser	Gln	Leu	Pro	Arg	Cys	His
			820					825					830		
Arg	Asn	Val	Phe	Arg	Tyr	Leu	Met	Ala	Phe	Leu	Arg	Glu	Leu	Leu	Lys
		835					840					845			
Phe	Ser	Glu	Tyr	Asn	Ser	Val	Asn	Ala	Asn	Met	Ile	Ala	Thr	Leu	Phe
	850					855					860				
Thr	Ser	Leu	Leu	Leu	Arg	Pro	Pro	Pro	Asn	Leu	Met	Ala	Arg	Gln	Thr
865					870					875					880
Pro	Ser	Asp	Arg	Gln	Arg	Ala	Ile	Gln	Phe	Leu	Leu	Gly	Phe	Leu	Leu
				885					890					895	
Gly	Ser	Glu	Glu	Asp											
				900											

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